

query (SEQ ID NO:1)
sequence1 (SEQ ID NO:2)
sequence2 (SEQ ID NO:3)
sequence3 (SEQ ID NO:4)
sequence4 (SEQ ID NO:5)
sequence5 (SEQ ID NO:6)
sequence6 (SEQ ID NO:7)
sequence7 (SEQ ID NO:8)

LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSQLTETSGDS-VTV
LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSQLTETSGDS-VTV
LVPFANFG-TVTFTGAEATTSSGTVTAADATLIDIEQNGEVLTSGST-VTV
LVQFANFG-TVTFTGASATQNGESVGVTGAQIIDLQDN-SVLTSGSTSSNS-VTV
LVNFADFD-TVTFKDCSPSVSG-----STIVDIRQSLEVTECSTTGTTVTC
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC

FIGURE 1

>P1;1b4k

structureX:1b4k: 10 :A : 335 :A :
YPYTRLRRNRRDDFSRRLVRENVLTVDDLILPVFVLGVNQRESIPSPMPGVERLSIDQLLIEAE
EWVALGIPALALFPVT:PVEKKSLDAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTH
GQDGILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMGRIGAIREALESAG:HTNVRIMAYSAKYASAYYGPFRDAVGSASNGLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGM
PYLDIVRRVK:DEFRAPTFVYQVSGEYAMHMGAIQNGWLAE:SVILESLTAFKragADGILTYFAKQAAEQLRR* (SEQ ID NO:9)

>P1;SC001

sequence:SC001: 13 : : 340 :
EISSVLAGGYNHPLLROWQSERQLTKNMLIFPLFISDNPDDTEIDSLPNINRIGVNRLKDYLK
PLVAKGLRSVILFGVPLIPGTKDGVTAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTS
GHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHKT
LSYAAKFSGNLYGPFRDAACSA:PSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPST
FYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEKGVVDLKTIAFESHQGFLRAGARLIITYL
APEFLDWLDE* (SEQ ID NO:10)

FIGURE 17

>P1;1a28
structureX: 1a28A : 701 : : 915 : :
AGHDNTKPDTSSSLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFLGWR SYKHVS
GQMLYFAPDLILNEQRMKESSFYSLCLTMW-QIPQEFVKLQVSQEEFLCMKVLLLNTI-PLEGLRSQTQFE
EMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRLSVEFPEMMSEVIA
A* (SEQ ID NO:11)
>P1;gi7766906
sequence: gi7766906 : 27 : : 233 :
EANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSSELPLDDQVILLRAGWNELLIASASHRSIA--V
KDGILLATGLHVHRNSAHSAGVGAI FDRVLTELVS KMRDMQM DKTEL GCLRAIVLFNPDS--KGLSNPAEVE
ALREKVYASLEAYCKHKYP--EQPGRFAKLLRLPALRSIGLKCLEHLFF-FKLIGDT--PIDTFLMEMLE
A* (SEQ ID NO:12)

FIGURE 20

>P1;1a28
structureX: 1a28A : 682 : : 921 : :
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSLLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQY
SWMSLMVFGLGWRSYKHVGQMLYFAPDLILNEQRMKE-SSFYSLCLTMWQIPQEfvKLQVSQEEFLCMKVL
LLLNL---TIPLEGLR---SQTQFEEMRSSYIRELIKAIQLRQKGVVSSQRFYQLTKLLDNLHDLVKQLHL
YCLNTFIQSRALSVEFPEMMSEVIAAQLPKIL* (SEQ ID NO:13)
sequence: gi3659931 : 14 : : 254 :
LTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLEC
AWLEILMIGLVWRSMEHP--GKLLFAPNLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSI
ILLNSGVYTFSLSTLKSLEEKDHIIHRVLDKITDTLIHLMAKAGLTQQQHERLAQLLLILSHIRHMSNKGME
HLYSMKCKN--VVPLYDLLLEMLD-AHR-LH* (SEQ ID NO:14)

FIGURE 24

>P1;1c3w
structureX: 1c3wA : 5 : : 231 : :
TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGE--
QN---PIYW-ARYADWLFTTPLLLALLVDADQGTILALVGADGIMIGTGLVGALTGVY--S--YRFVW
WAISTA-AMLYIILYVLFVGF----SMRPE-VA-STFKVLRNVTVVLWSAYPVVWLIGSEG---AGI---V
PLNIETLLFMVL-DVSAKVGFGILLRSRAIFG* (SEQ ID NO:15)
>P1;1e12A
sequence: 1e12A : 4 : : 236 :
ENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISYYLGLLSGLTVGMIEMPAGHA
LAGEMVRSQW-GRYLTWALSTPMILLALGLLADVDLGSLEFTVIAADIGMCVTGLAAAMTTS---ALLFRWAF
YAISCA-FFVVVLSALVTDWAASASSAGT--A--EIFDTLRVLTVVWLGYPIVWAVGV-----EGLALVQ
SVGATSWAYSVL-DVFAKYVFAFILLRWVANNE* (SEQ ID NO:16)

FIGURE 27

>P1;1f88
structureX: 1f88A : 37 : : 308 : :
FSMLAAYMFLLIMLGFPINFLTLVYVTQHKKLRT----PLNYILLNLAVALDFMVFGGFTTLYTSLHGYF
VFGPTGCNLEGFFATLGGEIALWSLVLAIERYVVVCKPMNSNFRFGENHAIMGVAFTWVMALACAAPPLVGW
SRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVFHIIPLIVIFFCYGQLVFTV-KEAAASATTQKAEKEV
TRMVIIMVIAFLICWL PYAGVAFYIFTHQGSDFGPIFMTI PAFFAKTSAVYNPVIYIM* (SEQ ID NO:17)
>P1;1c3wA
sequence: 1c3wA : 2 : : 215 : GRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYA-
ITTLVPAIAFTMYLSMLLGYGLTMVP-FGGEQ
-NPI-YWARYADWLFTPLLLLALLVDA-----D-----QGTILALVGADGIMIGTGLVGAL-----
TKVY-----SY-----RFVWWAISTAAMLYILYVLFFGFSMR--PEV-----ASTFKVL
RNVTVVVLWSAYPVVWLIGSEGAGI-----VPLNI--ETLLFMVLDVSAKVGFLILL* (SEQ ID NO:18)

FIGURE 29

>P1;6prc
structureX: 6prcL : 14 : : 258 : : GTLIGGDLFDFWVGPYFVGFFGVSAIFFIFLGVSLIGYAASQG-P---
---TW-DPFAISINPPDLKYGLG
A-APLLEGGFWQAITVCALGAFISWMLREVEISRKLIGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAPP
YGILSHLDWVNNFGYQYLNWYNPGHMSSVSFLFVNAMALGLHGGLILSVANP-GD----GD-----
-KVKTA-EHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRG* (SEQ ID NO:19)
>P1;6prcM
sequence: 6prcM : 34 : : 292 :
YSYWLKGKIGDAQIGPIYLGASGIAAAFAFGSTAILIILFNMAAEVHFDPQLQFFR--QFFWLGLYPPKAQYGMG
I-PPLHDGGWWLMAGLFMTLSLGSWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVP
FGIWPHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFG-----GDREIEQITDRG
T--AV--ERAALFWRWTFIGFNATIESVHRWGWFSLMVMVSASVGILLTGTFVDNW* (SEQ ID NO:20)

FIGURE 31

>P1;1qj8
structureX: 1qj8A : 4 : : 148 : :
TVTGGYAQSDAQGQM-NKMGGFNLKYRYEEDNSPLGVIGSFTYTE-K--SRTASSGDYN-KNQYYGITAGPA
YRINDWASIYGVVGVGYGYKFQTTEYPTYK-NDTSYGFSYGAGLQFNPMENVALDFSYEQRIRS-----
--VDVGTWIAGVGYRF* (SEQ ID NO:21)
>P1;1bxwA
sequence: 1bxwA : 19 : : 171 :
YHDTGLINNN--GPTHENKLGAGAFGGYQV-NPYVGFEMGYDWL--GRMPYKGSVENGAYKAQQVQLTAKLG
YPIITDDLDIYTRLGGMVWRADTY-SNVYGKNHTGVSPVFAAGGVEYAITPEIATRLEYQWTNNIGDAHTIGT
RP-DNGMLSLGVSYRF* (SEQ ID NO:22)

FIGURE 33

>P1;2por
structureX: 2por : 1 : : 301 :
EVKLSGDARMGVMYNGDD--WNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVG-----AETGEDGTV
FLSG-AFGKIEMGDALGASEALFGD--LYEVGYTDLDRGGNDIPYL-----TGDERLTAEDNPVLLYTY-
SA----GAFSVAASMS--DGKV-----GETSED-----DAQ---EMAVAAAYT-F--G
NY---TVGLGYEKIDSP-----DTAL-----MADMEQLELAIAIKFGATNVKAYYADGELDRDFARAV
FDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDVTVYYGLGASYDLGGGASIVGGIADNDL
PNSDMVADLGVKFKF* (SEQ ID NO:23)
>P1;1osmA
sequence: 1osmA : 10 : : 332 :
KLDLYGKIDGLHYFSDDKDVD-GDQTYMRLGVKGETQINDQLTGYGQWEYNVQ-ANNTTESSSDQAWTRLAFA
GLKFGDAGSFDYGRNYGVVY-DVTSWTDVLPE-----FGGDTY-----GSDNFLQSRANGVATYRN-
SDFFGLVDGLNFAHQY---QGKNGSVSSEGATNNRGAL---KQN-----GD---GFGTSVTYD-I--F
D---GISAGFAYANS-----KRTDDQNQLLGEGLDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSL-
-GFANKAQNFVEAAQYQFDGLRPSVAYLQSKGKDLNG-YGDQDILKYVDVGATYYFNKNMSTYVDYKINLL
DDNSFTRSAGISTDD* (SEQ ID NO:24)

FIGURE 35

P1;2mpr

structureX: 2mprA : 2 : : 427 : :

DFHGYARSGIGWTGS-----G---GEQQC-----FQA--TGAQS KYRLGNE-----
--CETYAELKLGQEVWKEGDKSFYFDTNVAYSVNQOND--WEST-DPAFREANVQGKNL--IEWLPGSTIW
AGKRFYQRHD--VHMIDFYYWDISGPAGAGIENIDLGFGLS-LAATRSTEAGGSYTFSSQNIYDEVKDTAN
DVFDVRLAGLQTNPDGVLELGVDYGRANTTDGYKL-ADGASKDGWMFTAETHQSMLKGYNKFVVQYATDAMT
TQGKGQARGSDGSSSFTEKINYANKVINNNG-NMWRILDHGAISLGDWKDLMYVGMYQNIWDNNL--GTEW
WTGVVRPMYKWTPIMSTLLEVGYDNVKS-QQ-----TGDRNNQYKITLA-QQ---WQAGDSIWSRPAIRI
FATYAKWDEKWKGYIKDGDNISRYAAAT-NSGISTNSRGDSDEWTFGAQMEIWW* (SEQ ID NO:25)

>P1;1a0tP

sequence: 1a0tP : 4 : : 413 :

EFHGYARSGIVMNDGASTKSGAYITPAGETGG-----AIGRL-----GNQ-----
--ADTYVEMNLEHKQTLDNGATTRFKVMVADGQTSYNDWTASTS-DLNVRQAFVELGNLPTFAGPFKGSTLW
AGKRF--DRDNFDIHWIDSDVVFLAGTGGGIYDVWKWNDGLRSNFSLYGRNFGDIDDSNSVQNYILTMNHFA
GPLQMMVSGLRAKDNDERKDSNG-NLAKGDAANTGV-----HALLGLHNDSFYGLRDGSSKTALLYG-HGLG
AEVKIGIGSDGA-----LRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQW
ATFNRLIQAQNQNFALAYEGSYQYMD--LKPEGYNDRQAVNGSFYKLTTF--APTFKVGSIGDFFSRPEIRF
YTSWMDWSKLNYYASDDALGS---DGF-----NSGGEWSFGVQMETWF* (SEQ ID NO:26)

FIGURE 37